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## In the Claims

The listing of claims will replace all prior versions and listing, of claims in the application:

## Listing of Claims:

1. (Original) A recombinant polynucleotide, the polynucleotide comprising a first and a second sequence, the first sequence encoding a signal peptide comprising a TAT signal and a Sec avoidance signal and the second sequence encoding a heterologous protein, wherein the sequence of the signal peptide is

 $M-X_1-K/R-X_2-K/R-X_3-RR-X_4-K/R-A$ 

in which  $X_1$  is a sequence of 0 to 10 amino acids;  $X_2$  is a sequence of 0 to 3 amino acids;  $X_3$  is a sequence of 0 to 10 amino acids; and  $X_4$  is a sequence of 15 to 24 amino acids in which at least 75% up to about 90% of the residues are hydrophobic.

- 2. (Original) A recombinant polynucleotide according to claim 1 wherein  $X_1$  is a sequence of 0 to 5 amino acids, and is preferably 0.
- 3. (Currently Amended) A recombinant polynucleotide according to claim 1 or 2 wherein  $X_2$  is a sequence of 0 or 1 amino acid, preferably 0.
- 4. (Currently Amended) A recombinant polynucleotide according to any one of claims  $1 \ \text{to} \ 3$  claim 1 wherein  $X_3$  is a sequence of 0 to 5 amino acids, preferably 0.
- 5. (Currently Amended) A recombinant polynucleotide according to any one of claims 1 to 4 claim 1 wherein  $X_4$  is a sequence of at least 20 amino acids of which at least 18 are hydrophobic amino acids.

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- 6. (Currently Amended) A recombinant polynucleotide according to any one of claims 1 to 5 claim 1 wherein  $X_4$  is 23 amino acids.
- 7. (Currently Amended) A recombinant polynucleotide according to any one of claims 1 to 6 claim 1 wherein the sequence of the signal peptide is MKKRRVVNSVLLLLLLASALALTVAPMAKA (SEQ ID NO:1).
- 8. (Original) A signal peptide, the signal having the sequence

 $M-X_1-K/R-X_2-K/R-X_3-RR-X_4-K/R-A$ .

- in which  $X_1$  is a sequence of 0 to 10 amino acids;  $X_2$  is a sequence of 0 to 3 amino acids;  $X_3$  is a sequence of 0 to 10 amino acids; and  $X_4$  is a sequence of 15 to 24 amino acids in which at least 75% up to about 90% of the residues are hydrophobic.
- 9. (Original) A signal peptide according to claim 8 wherein  $X_1$  is a sequence of 0 to 5 amino acids, and is preferably 0.
- 10. (Currently Amended) A signal peptide according to claim 8 erg 9 wherein  $X_2$  is a sequence of 0 to 1 amino acid, preferably 0.
- 11. (Currently Amended) A signal peptide according to any one of claims 8 to 10 claim 8 wherein  $X_3$  is a sequence of 0 to 5 amino acids, preferably 0.
- 12. (Currently Amended) A signal peptide according to any one of claims 8 to 11 claim 8 wherein  $X_4$  is a sequence of at least 20 amino acids of which at least 18 are hydrophobic amino acids.

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- 13. (Currently Amended) A signal peptide according to any one of claims 8 to 12 claim 8 wherein  $X_4$  is 23 amino acids.
- 14. (Currently Amended) A signal peptide according to any one of claims 8 to 13 claim 8 wherein the sequence of the signal peptide is MKKRRVVNSVLLLLLLASALALTVAPMAKA (SEQ ID NO 1).
- 15. (Original) A method of producing a heterologous polypeptide from a host cell comprising a TAT translocation system, the method comprising:
  - (i) transforming the host cell with a DNA sequence encoding the heterologous polypeptide and a signal peptide wherein the signal peptide comprises a TAT signal and a Sec avoidance signal wherein the sequence of the signal peptide is

 $M-X_1-K/R-X_2-K/R-X_3-RR-X_4-K/R-A$ 

- in which  $X_1$  is a sequence of 0 to 10 amino acids;  $X_2$  is a sequence of 0 to 3 amino acids;  $X_3$  is a sequence of 0 to 10 amino acids; and  $X_4$  is a sequence of 15 to 24 amino acids in which at least 75% up to about 90% of the residues are hydrophobic.
- (ii) culturing the host cell under conditions which allow expression of the heterologous polypeptide; and
- (iii) recovering the heterologous polypeptide secreted from the host cell via the TAT translocation system.
- 16. (Original) A method according to claim 15 wherein  $X_i$  is sequence of 0 to 5 amino acids, and is preferably 0.

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- 17. (Currently Amended) A method according to claim 15  $\frac{16}{16}$  wherein  $X_2$  is a sequence of 0 or 1 amino acid, preferably 0.
- 18. (Currently Amended) A method according to any one of claims 15 to 17 claim 15 wherein  $X_3$  is a sequence of 0 to 5 amino acids, preferably 0.
- 19. (Currently Amended) A method according to any one of claims 15 to 18 claim 15 wherein  $X_4$  is a sequence of at least 20 amino acids of which at least 18 are hydrophobic amino acids.
- 20. (Currently Amended) A method according to any one of claims 15 to 19 claim 15 wherein  $X_4$  is 23 amino acids.
- 21. (Currently Amended) A method according to any one of claims 15 to 20 claim 15 wherein the sequence of the signal peptide is MKKRRVVNSVLLLLLLASALALTVAPMAKA (SEQ ID NO:1).
- 22. (Currently Amended) A method according to any one of claims 15 to 21 claim 15 wherein the host cell is Bacillus sp.
- 23. (Original) A method according to claim 22 wherein the host cell is selected from the group consisting of Bacillus choshinensis, Bacillus brevis, Bacillus subtilis, Bacillus licheniformis, and Bacillus megatorium.
- 24. (Original) A method according to claim 22 wherein the host cell is Bacillus choshinensis.
- 25. (Currently Amended) A method according to any one of claims 15 to 24 claim 15 wherein the heterologous polypeptide is a polypeptide which readily folds in the cytoplasm.

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26. (Currently Amended) A method according to any one of claims 15 to 25 claim 15 wherein the polynucleotide encoding the mature polypeptide has a sequence selected from:

- (i) a sequence of nucleotides shown in SEQ ID NO:29 from nucleotide 85 to 1155;
- (ii) a sequence that hybridises to SEQ ID NO:29
   from nucleotide 85 to 1155 under conditions
   of high stringency;
- (iii) a sequence which is greater than 90%
  identical to SEQ ID NO:29 from nucleotide 85
  to 1155; and
- (iv) a sequence that encodes the amino acid sequence provided in SEQ ID NO:30 from residue 29 to 384.
- 27. (Currently Amended) A method according to any one of claims 15 to 25 claim 15 wherein the mature heterologous polypeptide comprises the sequence provided in SEQ ID NO:30 from residue 29 to 384; or a polypeptide which is greater than 90% identical to the sequence provided in SEO ID NO:30.
- 28. (Currently Amended) A substantially purified polypeptide produced according to the method of any of claims 15 to 27 claim 15.
- 29. (Currently Amended) A vector comprising the recombinant polynucleotide according to any of claims 1 to 8 claim 1.
- 30. (Currently Amended) A host cell comprising the recombinant polynucleotide according to any of claims 1 to 8 claim 1.